

PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN ANALYSIS

Abstract

Disclosed are methods for reliably detecting the presence of proteins, especially
5 proteins with various post-translational modifications (phosphorylation, glycosylation, methylation, acetylation, etc.) in a sample by the use of one or more capture agents that recognize and interact with recognition sequences uniquely characteristic of a set of proteins (Proteome Epitope Tags, or PETs) in the sample. Arrays comprising these capture agents or PETs are also provided.